

H		gagtctaacacggaccaaggagtttaac
M	-60	tgaaaagatagaataaatggcctcgtgc
H		M E W P A R L C G
		ATGGAGTGGCCGGCGCGGCTCTGCGGGC
		* * * *
M	1	ATGGCGCGGCCAGCGCTGCTGGGCGAGC
M	1	M A R P A L L G E
H		G G G G A P T E T
H		GGGGGCGGGGGCGCGCCTACGGAAACTC
		* * * *
M	61	GGCCAAGTTGCCGCGGCCACAGAAGTTC
M	21	G Q V A A A T E V
H		E N L C T V I W T
H		GAAAACCTCTGCACAGTAATATGGACAT
		* * * * * * *
M	121	GAAAATCTCTGCACGATAATATGGACGT
M	41	E N L C T I I W T
H		S L W Y F S H F G
H		AGTCTATGGTATTTTAGTCATTTTGGCG
		* * * * *
M	181	ACTCTCAGATATTTTAGTCACTTTGATG
M	61	T L R Y F S H F D

Fig. 7A

```

acgtgcggccgggttcgcgagggcgagaggctgc
    ....
cgaattcggcacgagccgagggcgaggggcctgc

L  W  A  L  L  L  C  A  G  G  G  G
TGTGGGCGCTGCTGCTCTGCGCCGGCGGGGGGC
*      *  *  *
TGTGTGGTGCTGCTACTGTGGACCGCCACCGTG---
L  L  V  L  L  L  W  T  A  T  V  -

Q  P  P  V  T  N  L  S  V  S  V
AGCCACCTGTGACAAATTTGAGTGTCTCTGTT
*  *  *  *  *  *  *  *  *  *  *
AGCCACCTGTGACGAATTTGAGCGTCTCTGTC
Q  P  P  V  T  N  L  S  V  S  V

W  N  P  P  E  G  A  S  S  N  C
GGAATCCACCCGAGGGAGCCAGCTCAAATTGT
*      *  *  *  *  *  *      *  *
GGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC
W  S  P  P  E  G  A  S  P  N  C

D  K  Q  D  K  K  I  A  P  E  T
ACAAACAAGATAAGAAAATAGCTCCGGAAACT
*      *  *  *  *  *  *  *  *
ACCAACAGGATAAGAAAATTGCTCCAGAAACT
D  Q  Q  D  K  K  I  A  P  E  T
    
```

Fig. 7B

H		R	R	S	I	E	V	P	L	N																						
H		C	G	T	C	G	T	T	C	A	T	A	G	A	A	G	T	A	C	C	C	T	G	A	A	T	G					
		*				*			*			*			*			*			*											
M	241	C	A	T	C	G	T	A	A	A	G	A	G	A	T	T	A	C	C	C	C	T	G	G	A	T	G					
M	81	H	R	K	E	E	L	P	L	D																						
H		S	T	N	E	S	E	K	P	S																						
H		A	G	C	A	C	A	A	T	G	A	G	A	G	T	G	A	G	A	A	G	C	C	T	A	G	C	A				
		*		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*				
M	301	A	G	T	G	C	C	A	A	T	G	A	A	A	G	T	G	A	G	A	A	G	C	C	T	A	G	C				
M	101	S	A	N	E	S	E	K	P	S																						
H		G	D	P	E	S	A	V	T	E																						
H		G	G	T	G	A	T	C	C	T	G	A	G	T	C	T	G	C	T	G	T	G	A	C	T	G	A	A	C			
		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*				
M	361	G	G	T	G	A	T	C	C	T	G	A	G	T	C	C	G	C	T	G	T	G	A	C	T	G	A	G	C			
M	121	G	D	P	E	S	A	V	T	E																						
H		K	C	S	W	L	P	G	R	N																						
H		A	A	G	T	G	T	T	C	T	T	G	G	C	T	C	C	C	T	G	G	A	A	G	G	A	A	T	A			
		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*				
M	421	A	A	G	T	G	T	T	C	T	T	G	G	C	T	C	C	C	T	G	G	A	A	G	G	A	A	T	A			
M	141	K	C	S	W	L	P	G	R	N																						
H		W	H	R	S	L	E	K	I	H																						
H		T	G	G	C	A	C	A	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	T	T	C	A	T	C

Fig. 7C

E R I C L Q V G S Q C
AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT
* * * * *
AGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
E K I C L Q V G S Q C

I L V E K C I S P P E
TTTTGGTTGAAAAATGCATCTCACCCCCAGAA
* * * * *
CTTTGGTGAAAAAGTGCATCTCACCCCCCTGAA
P L V K K C I S P P E

L Q C I W H N L S Y M
TTCAATGCATTTGGCACAACCTGAGCTACATG
* * * * *
TCAAGTGCATTTGGCATAACCTGAGCTATATG
L K C I W H N L S Y M

T S P D T N Y T L Y Y
CCAGTCCCGACACTAATACTCTCTACTAT
* * * * *
CAAGCCCTGACACACTATACTCTGTACTAT
T S P D T H Y T L Y Y

Q C E N I F R E G Q Y
AATGTGAAAACATCTTTAGAGAAGGCCAATAC

Fig. 7D

			*		*	*	*	*	*
M	481	TGGTACAGCAGCCTGGAGAAAAGTCGTC							
M	161	W Y S S L E K S R							
H		F G C S F D L T K							
H		TTTGGTTGTTTCCTTTGATCTGACCAAAG							
			*	*	*		*	*	*
M	541	ATTGCTTGTTTCCTTTAAATTGACTAAAG							
M	181	I A C S F K L T K							
H		Q I M V K D N A G							
H		CAAATAATGGTCAAGGATAATGCAGGAA							
			*	*	*	*	*	*	*
M	598	CAAATAATGGTCAAGGATAATGCTGGGA							
M	200	Q I M V K D N A G							
H		T S R V K P D P P							
H		ACTTCCCCTGTGAAACCTGATCCTCCAC							
			*	*		*	*	*	*
M	658	ACTTCCTATGTGAAACCTGATCCTCCAC							
M	220	T S Y V K P D P P							
H		L Y V Q W E N P Q							
H		CTATATGTGCAATGGGAGAATCCACAGA							
			*		*	*	*	*	*
M	718	TTATTAGTGCAGTGGAAGAATCCACAAA							
M	240	L L V Q W K N P Q							

Fig. 7E

```
* * * * * * * * *
AATGTGAAAACATCTATAGAGAAGGTCAACAC
Q C E N I Y R E G Q H

V K D S S F E Q H S V
TGAAGGATTCCAGTTTGAACAACACAGTGTC
* * * * *
TGGAACCT - - AGTTTGAACATCAGAACG TT
V E P - S F E H Q N V

K I K P S F N I V P L
AAATTAAACCATCCTTCAATATAGTGCCTTTA
* * * * *
AAATTAGGCCATCCTGCAAAATAGTGTCTTTA
K I R P S C K I V S L

H I K N L S F H N D D
ATATTAAAAACCTCTCCTTCCACAATGATGAC
* * * * *
ATATTAAACATCTTCTCCTCAAAAATGGTGCC
H I K H L L L K N G A

N F I S R C L F Y E V
ATTTTATTAGCAGATGCCTATTTTATGAAGTA
* * * * *
ATTTTAGAAGCAGATGCTTA ACTTATGAAGTG
N F R S R C L T Y E V
```

Fig. 7F

H		E	V	N	N	S	Q	T	E	T
H		GAAGTCAATAACAGCCAAACTGAGACAC								
		*	*	*	*		*	*		
M	778	GAGGTCAATAATACTCAAACCGACCGAC								
M	260	E	V	N	N	T	Q	T	D	R
H		E	N	P	E	F	E	R	N	V
H		GAGAATCCAGAA'TTTGAGAGAAATGTGG								
		*		*			*	*		
M	838	CAGAATTCCGAATCTGATAGAAACATGG								
M	280	Q	N	S	E	S	D	R	N	M
H		L	P	D	T	L	N	T	V	R
H		CTTCCTGATACTTTGAACACAGTCAGAA								
		*		*			*	*	*	
M	898	CTTGCCGACGCTGTCTACACAGTCAGAG								
M	300	L	A	D	A	V	Y	T	V	R
H		D	D	K	L	W	S	N	W	S
H		GATGACAAACTCTGGAGTAATTGGAGCC								
		*		*	*	*	*	*	*	*
M	958	GACAACAAACTGTGGAGTGATTGGAGTG								
M	320	D	N	K	L	W	S	D	W	S
H		T	L	Y	I	T	M	L	L	I
H		ACACTCTACATAACCATGTTACTCATTG								

Fig. 7G

H N V F Y V Q E A K C
ATAATGTTTCTACGTCCAAGAGGCTAAATGT
* * * * *
ATAATATTTTAGAGGTTGAAGAGGACAAATGC
H N I L E V E E D K C

E N T S C F M V P G V
AGAATACATCTTGTTTCATGGTCCCTGGTGTT
* * * * *
AGGGTACAAGTTGTTTCCAACCTCCCTGGTGTT
E G T S C F Q L P G V

I R V K T N K L C Y E
TAAGAGTCAAAACAAATAAGTTATGCTATGAG
* * * * *
TAAGAGTCAAAACAAACAAGTTATGCTTTGAT
V R V K T N K L C F D

Q E M S I G K K R N S
AAGAAATGAGTATAGGTAAGAAGCGCAATTCC
* * * * *
AAGCACAGAGTATAGGTAAGGAGCAAAACTCC
E A Q S I G K E Q N S

V P V I V A G A I I V
TTCCAGTCATCGTCGCAGGTGCAATCATAGTA

Fig. 7H

			*	*	*	*	*	*	*
M	1018	ACCTTCTACACCACCATGTTACTCACCA							
M	340	T F Y T T M L L T							
H		L L L Y L K R L K							
H		CTCCTGCTTTACCTAAAAAGGCTCAAGA							
		* * * * *							
M	1078	CTCCTT TTTTACCTGAAAAGGCTTAAGA							
M	360	L L F Y L K R L K							
H		K I F K E M F G D							
H		AAGATTTTAAAGAAATGTTTGGAGACC							
		* * * * *							
M	1138	AAGATTTTAAAGAAATGTTTGGAGACC							
M	380	K I F K E M F G D							
H		D I Y E K Q T K E							
H		GACATCTATGAGAAGCAAACCAAGGAGG							
		* * * * *							
M	1198	GACATCTATGAGAAACAATCCAAAGAAG							
M	400	D I Y E K Q S K E							
H		K K A S Q *							
H		AAGAAAGCCTCTCAGTGAtggagataat							
		* * *							
M	1258	AAGAAAGCAGCTCCTTGAtgggggagaag							
M	420	K K A A P *							

Fig. 7I

```
      *      *      *      *      *      *
TTCCAGTCCTTTGTGCGCAGTGGCAGTCATAATC
I  P  V  F  V  A  V  A  V  I  I

I  I  I  F  P  P  I  P  D  P  G
TTATTATATTCCCTCCAATTCCTGATCCTGGC
*  *  *  *  *  *  *  *  *  *  *
TCATTATATTTTCCTCCAATTCCTGATCCTGGC
I  I  I  F  P  P  I  P  D  P  G

Q  N  D  D  T  L  H  W  K  K  Y
AGAATGATGATACTCTGCACTGGAAGAAGTAC
*  *  *  *  *  *  *  *  *  *  *
AGAATGATGATACCCTGCACTGGAAGAAGTAT
Q  N  D  D  T  L  H  W  K  K  Y

E  T  D  S  V  V  L  I  E  N  L
AAACCGACTCTGTAGTGCTGATAGAAAACCTG
*  *  *  *  *  *  *  *  *  *  *
AAACGGATTCTGTAGTGCTGATAGAAAACCTG
E  T  D  S  V  V  L  I  E  N  L

ttatttttaccttcactgtgaccttgagaaga
tgattttctttcttgccttcaatgtgaccctgt
```

Fig. 7J